### SEQUENCE LISTING

(1)	GENERAL	INFORMATION:
( _ /	GHMHM	TIVE ORGERITATION.

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- (A) NAME: Yi Sun (B) STREET: 4841 Hillway Court
- (C) CITY: Ann Arbor
  (D) STATE: Michigan
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 48105 (G) TELEPHONE: (313) 996-1959 (H) TELEFAX: (313) 996-7158

- (ii) TITLE OF INVENTION: Sensitive to Apoptosis Gene (SAG)
- (iii) NUMBER OF SEQUENCES: 50
- (iv) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk

  - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

# (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1140 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 17..355
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
    (B) LOCATION:17..355
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1...1140
  - (D) OTHER INFORMATION:/note= "Mouse SAG"

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTTC	CTGCC	GCC (	GCCG(						AG GA Lu As 5				lu Pi			49
GTC Val	CTT Leu	TCT Ser	TCG Ser 15	CAC His	TCC Ser	GGG Gly	AGC Ser	GCA Ala 20	GGC Gly	TCC Ser	AAG Lys	TCG Ser	GGA Gly 25	GGC Gly	GAC Asp	97
AAG Lys	ATG Met	TTC Phe 30	TCT Ser	CTC Leu	AAG Lys	AAG Lys	TGG Trp 35	AAC Asn	GCG Ala	GTA Val	GCC Ala	ATG Met 40	TGG Trp	AGC Ser	TGG Trp	145
GAC Asp	GTT Val 45	GAG	TGC Cys	GAT Asp	ACC Thr	TGT Cys 50	GCC Ala	ATC Ile	TGC Cys	AGG Arg	GTC Val 55	CAG Gln	GTG Val	ATG Met	GAT Asp	193
									AAG Lys							241
GTC Val	TGG Trp	GGA Gly	GAG Glu	TGT Cys 80	AAC Asn	CAT His	TCC Ser	TTC Phe	CAC His 85	AAC Asn	TGC Cys	TGC Cys	ATG Met	TCC Ser 90	CTG Leu	289

TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val 95 100 105	337
GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG Val Gln Arg Ile Gly Lys 110	385
TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT	445
GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTTGG	505
GAAATTCTCT ACAATTAAGA TAATTTGTTA AAAATGGCCT TTCCTACCTC TGGTGTGTGT	565
GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC	625
CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG TGTTTATGCT TGAGGGTTAA	685
AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT	745
AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG	805
AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT GTCGGGTAAA CTGTAATATG	865
GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTTGAC TTGGCCAGGA	925
AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTTG CCGAAGGTTG	985
TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG	1045
TTCATTATGC AATGTTTTAA TAAAATATTG TGCTTTGAGT TATTAAAGTT TGATATATAC	1105
TCTTAAAATC ATTAAACTAA TTCATCAATT AAATG	1140

# (2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His

Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

# (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 754 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double (D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: cDNA

(ix) FEAT	JRE	:
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- (A) NAME/KEY: CDS (B) LOCATION:1..339

# (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
  (B) LOCATION:1..339

# (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
  (B) LOCATION:1..754
  (D) OTHER INFORMATION:/note= "Human SAG"

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

				GAA Glu 5													48
TCC Ser	GGG Gly	AGC Ser	TCA Ser 20	GGC Gly	TCC Ser	AAG Lys	TCG Ser	GGA Gly 25	GGC Gly	GAC Asp	AAG Lys	ATG Met	TTC Phe 30	TCC Ser	CTC Leu		96
				GCG Ala												. 1	44
				TGC Cys												1	.92
				AAA Lys												2	240
				CAC His 85												2	888
AAT Asn	CGC Arg	TGC Cys	CCT Pro 100	CTC Leu	TGC Cys	CAG Gln	CAG Gln	GAC Asp 105	TGG Trp	GTG Val	GTC Val	CAA Gln	AGA Arg 110	ATC Ile	GGC Gly	3	336
AAA Lys	TGAG	GAGT	GGT 1	raga	AGGC	rt C	rtag(	CGCA	G TT(	GTTC	AGAG	CCC	rggto	GGA		3	889
TCT	rgtai	ATC (	CAGT	GCCC'	ra c	AAAG	GCTA	G AAG	CACT	ACAG	GGG	ATGA	TTA	CTTC	AAATAG	4	149
GAG	CCGA	rgg z	ATCT	GTGG'	rc t'	rtgg/	ACTC	A TC	AAAG	CCTT	GGT	ragc <i>i</i>	ATT '	rgtc2	AGTTTT	5	509
ATC	TTCA	GAA A	ATTC'	TCTG'	rg a'	TAA	GAAG	A TA	ATTT	ATTA	AAG	GTGG'	rcc '	rtcc:	PACCTC	5	569
TGT	GTG!	rgt (	GTCG	CGCA	CA C	AGCT'	raga.	A GT	GCTA'	FAAA	AAA	GGAA	AGA (	GCTC	CAAATT	6	529
GAA'	rcac	CTT A	ATAA'	TTTA	CC C	ATTT	CTAT	A CA	ACAG	GCAG	TGG	AAGC	AGT '	rtcg/	AGACTT	6	589
TTT	CGAT	GCT 1	TATG	GTTG.	AT C	AGTT	AAAA	A AG	AATG'	ГТАС	AGT	AACA	AAT I	AAAG'	TGCAGT	7	749
TTA	AA															7	754

# (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met 1	Ala	Asp	Val	Glu 5	Asp	Gly	Glu	Glu	Thr 10	Cys	Ala	Leu	Ala	Ser 15	His		
Ser	Gly	Ser	Ser 20	Gly	Ser	Lys	Ser	Gly 25	Gly	Asp	Lys	Met	Phe 30	Ser	Leu		٠
Lys	Lys	Trp 35	Asn	Ala	Val	Ala	Met 40	Trp	Ser	Trp	Asp	Val 45	Glu	Cys	Asp		
Thr	Cys 50	Ala	Ile	Cys	Arg	Val 55	Gln	Val	Met	Asp	Ala 60	Cys	Leu	Arg	Cys		
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80		
Asn	His	Ser	Phe	His 85	Asn	Cys	Cys	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn		
Asn	Arg	Cys	Pro 100	Leu	Cys	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly		
Lys																	
(2)	INFO	ORMA'	rion	FOR	SEQ	ID I	: OV	5:									
	(i)	() () ()	QUENCA) LIB) TO	ENGTI YPE : TRANI	H: 1 nuci DEDNI	B bas leic ESS:	se pa acio sino	airs 1									
	(ii								ic a		1010	o tid	n D1				
d	ownst		m pr			JN:	/ue:	sc –	"ol:	rgom	исте	JULU	s Fi				
	(xi	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ :	ID N	O: 5	:						
AAG	CTTT	rtt '	TTTT	TTTR												18	3
(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	10:	5:									
	(i)	(, (; ()	QUENCA) L' B) T' C) S' D) T	ENGT YPE: TRAN	H: 1 nuc DEDN	3 ba: leic ESS:	se pa acio sin	airs d									
	(ii	) MO:	LECU	LE T	YPE:	oth	er n	ucle: sc =	ic a "Ol	cid igon	ucle	otid	e: P	2			
u;	pstr		prim				,			- 3							
	(xi	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0: 6	:						
AAG	CTTNI	NNN :	NNN													13	3
(2)	INF	ORMA	TION	FOR	SEQ	ID :	NO:	7:									
	(i	(. (. (.	QUENCA) L: B) T C) S' D) T	ENGT YPE : TRAN	H: 2 nuc DEDN	5 ba leic ESS:	se p aci sin	airs d									
	(ii	) MO	LECU A) D	LE T ESCR	YPE: IPTI	oth ON:	er n /de	ucle sc =	ic a "Ol	cid igon	ucle	otid	e SA	G TA	.01"		

	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
CGG	GATCC	CC ATGGCCGACG TGAGG	25
(2)	INFO	RMATION FOR SEQ ID NO: 8:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
•	(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG T.02"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
CGG	GATCC'	TC ATTTGCCGAT TCTTTG	26
(2)	INFO	RMATION FOR SEQ ID NO: 9:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 26 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide P.01"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
TAT	GGCTA	GC ATGGCCGACG TGGAGG	26
(2)	INFO	RMATION FOR SEQ ID NO: 10:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 16 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: peptide	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
	Gln 1	Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg 5 10 15	
(2)	INFO	RMATION FOR SEQ ID NO: 11:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 747 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(ix)	FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1270	

(ix) FEATURE:

### (A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..270

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:	11:
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ATG Met 1	GCC Ala	GAC Asp	GTG Val	GAA Glu 5	GAC Asp	GGA Gly	GAG Glu	GAA Glu	ACC Thr 10	TGC Cys	GCC Ala	CTG Leu	GCC Ala	TCT Ser 15	CAC His	48
															CTC Leu	96
AAG Lys	AAG Lys	TGG Trp 35	AAC Asn	GCG Ala	GTG Val	GCC Ala	ATG Met 40	TGG Trp	AGC Ser	TGG Trp	GAC Asp	GTG Val 45	GAG Glu	TGC Cys	GAT Asp	144
ACG Thr	TGC Cys 50	GCC Ala	ATC Ile	TGC Cys	AGG Arg	GTC Val 55	CAG Gln	ATG Met	CCT Pro	GTC Val	TTA Leu 60	GAT Asp	GTC Val	AAG Lys	CTG Leu	192
														ATC Ile	ATT Ile 80	240
			ACT Thr							TGA	AACA	GAA (	CAAT	CGCT	GC	290
ССТС	TCTC	GCC 2	AGCA	GGAC'	rg g	GTGG'	rcca.	A AG	AATC	GGCA	AAT	GAGA	GTG (	GTTA	GAAGGC	350
ттст	TAG	CGC 2	AGTT	GTTC	AG A	GCCC'	rggT(	G GA	rctt(	GTAA	TCC	AGTG	ccc '	TACA	AAGGCT	410
AGAA	CAC	rac .	AGGG	GATG	AA T'	rctt	CAAA'	r AG	GAGC	CGAT	GGA'	rctg'	rgg '	TCTT'	rggaci	r 470
CATO	CAAAC	GCC '	TTGG'	TTAG	CA T	TTGT	CAGT'	r tt	ATCT'	rcag	AAA'	TTCT(	CTG '	TGAT'	raaga <i>i</i>	A 530
GATA	ATT	TAT '	TAAA	GGTG	GT C	CTTC	CTAC	C TC	rgtg	GTGT	GTG'	rcgc	GCA (	CACA	GCTTAC	590
AAGT	GCT	ATA .	AAAA	AGGA	AA G.	AGCT	CCAA	A TT	GAAT	CACC	TTA'	TAAT'	TTA	CCCA'	TTTCT?	4 650
TACA	AACA	GGC .	AGTG	GAAG	CA G	TTTC	GAGA	C TT	TTTC	GATG	CTT	ATGG'	TTG .	ATCA	GTTAA	A 710
AAAC	SAAT	GTT .	ACAG'	TAAC	AA A	TAAA	GTGC.	A GT	TTAA	A						747

### (2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 90 amino acids(B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp \$45\$

Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu 50 60

Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile 65 70 75 80

Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly 85 90

(2) INFORMATION FOR SEQ ID NO: 13:

(i)	SEQUENCE	CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

#### (ii) MOLECULE TYPE: cDNA

# (ix) FEATURE:

- (A) NAME/KEY: CDS
  (B) LOCATION:1..291

# (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide (B) LOCATION:1..291

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

	•
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15	48
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 · 25 30	96 1
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GTG GTC TGG GGA GAA TGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys 50 60	192
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 65 70 75	ì
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 85	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys	341
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAAT	TAG 401
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTT	гтт 461
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACC	CTC 521
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAA	ATT 581
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGAC	CTT 641
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCA	AGT 701
TTAAA	706

# (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1				5					10					15		
Ser	Gly	Ser	Ser 20	Gly	Ser	Lys	Ser	Gly 25	Gly	Asp	Lys	Met	Phe 30	Ser	Leu	
Lys	Lys	Trp 35	Asn	Ala	Val	Ala	Met 40	Trp	Ser	Trp	Asp	Val 45	Glu	Cys	Asp	
Thr	Cys 50	Ala	Ile	Суѕ	Arg	Val 55	Gln	Val	Met	Val	Val 60	Trp	Gly	Glu	Cys	
Asn 65	His	Ser	Phe	His	Asn 70	Cys	Cys	Met	Ser	Leu 75	Trp	Val	Lys	Gln	Asn 80	
Asn	Arg	Cys	Pro	Leu 85	Cys	Gln	Gln	Asp	Trp 90	Val	Val	Gln	Arg	Ile 95	Gly	
Lys																
(2)	(i)	) SE( (A (I (C (I	QUENCA) LI B) T' C) S' C) TC	FOR CE CI ENGTI YPE: TRANI OPOLO LE T' ESCR	HARACH: 18 nuc: DEDNI DGY:	CTER: 3 bas leic ESS: line	ISTIC se pa acic sing ear	CS: airs d gle ucle:		cid igon	ucleo	otide	e hS <i>i</i>	AG. 1	M1"	
	(xi)	) SE(	QUEN	CE D	ESCR:	IPTI(	ON: S	SEQ :	ID N	O: 1!	ō:					
GCC	ATCTO	GCA (	GGGT(	CCAG												18
(2)	INF	ORMA!	rion	FOR	SEQ	ID I	10:	16:								
	(i)	( I ( I	A) L: B) T: C) S'	CE CI ENGTI YPE: TRANI	H: 2' nuc DEDNI	7 ba: leic ESS:	se pa acio sino	airs d								
	(ii			LE T' ESCR						cid igon	uċle	otide	e SA	G T.	02L"	
	(xi	) SE(	QUEN	CE D	ESCR:	IPTI	ON:	SEQ :	ID N	0: 1	6:					
GGA:	CCT	CAT :	rtgc(	CGAT'	TC T'	rtgg:	AC									27
(2)	INF	ORMA!	TION	FOR	SEQ	ID I	NO:	17:								
	(i)	( ) ( ) ( )	A) L: B) T' C) S'	CE C ENGT YPE: TRAN	H: 5: nuc: DEDNI	B bas leic ESS:	se pacionsing	airs d								
SI	•		A) D	LE T						cid igon	ucle	otid	е			
	(xi	) SE	QUEN	CE D	ESCR:	IPTI(	ON:	SEQ :	ID N	0: 1	7:					

58

TTCTCCAGTG GCAGAGAACT TTAAAGAGAA ATAGTTCAAC CGTACGCTGC AGGTCGAC

(2) INFORMATION FOR SEQ ID NO: 18:

	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 59 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
4 -	(ii) -3"	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAGKan MX	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
ACC	CGGT	AT GATTTAAATG TTTACGGGCA ATTCATTTTT ATCGATGAAT TCGAGCTCG	59
(2)	INFO	RMATION FOR SEQ ID NO: 19:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 19 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 5"	
	(vi)	SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
			19
TTC'	I'CCAG'	TG GCAGAGAAC	19
(2)	INFO	RMATION FOR SEQ ID NO: 20:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 3"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
ATG	ATTTA.	AA TGTTTACGGG C	21
(2)	INFO	RMATION FOR SEQ ID NO: 21:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(ix)	FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1339	
	(ix)	FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION:1339	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 21:	

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						GGA										48
						AAG Lys									CTC Leu	96
						GCC Ala										144
						GTC Val 55										192
						GAG Glu										240
						TGC Cys										288
						CAG Gln									GGC Gly	336
AAA Lys	TGAG	GAGT(	GGT 1	raga <i>i</i>	AGGC!	rt C	rtag(	CGCA	G TTC	GTTC?	AGAG	CCC	rggt	GGA		389
TCTT	rgta?	ATC (	CAGT	GCCC	ra cz	AAAG	CTAC	G AAC	CACTA	ACAG	GGG	ATGA	ATT (	CTTC	AAATAC	449
GAG	CCGA	rgg 2	ATCT	GTGG:	rc T	rtgg/	ACTC	A TC	AAAGO	CTT	GGT	rage:	TTA	TGTC!	AGTTTT	509
ATCI	TCAC	GAA A	ATTC:	rctg:	rg ar	rtaa(	GAAGA	A TA	ATTT?	ATTA	AAG	GTGG'	rcc '	TTCC	гассто	569
TGT	GTG	rgt (	GTCG	CGCA	CA C	AGCT	raga <i>i</i>	A GTO	GCTA:	FAAA	AAA	GGAA	AGA (	GCTC	CAAATT	629
GAAT	CAC	CTT A	ATAA	PTTA	CC CZ	ATTT(	CTATA	A CAZ	ACAG	GCAG	TGG	AAGC	AGT '	TTCG2	AGACTT	689
тттс	CGATO	GCT '	ratg(	GTTG2	AT C	AGTT	AAAA	A AG	AATG:	TAC	AGT	AACA	AAT .	AAAG'	rgcagi	749
ጥጥል	AΑ															754

# (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

Gln Ala Glu As<br/>n Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

100 105 110

Lys

(2) IN	FORMATION	FOR	SEO	ID	NO:	23:
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- (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 754 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
    (B) LOCATION:1..339
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
    (B) LOCATION:1..339

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15	48
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	144
ACG TGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60	192
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	240
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95	288
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110	336
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys	389
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys
65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110

Lys

- (2) INFORMATION FOR SEQ ID NO: 25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 754 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1...339
  - (ix) FEATURE:
    - (A) NAME/KEY: mat\_peptide
    - (B) LOCATION:1..339
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His	
1				5					10					15		

TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC	96
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu	
	_		20					25					30			

AAG AAG TGG	AAC GCG GTG	GCC ATG TGG A	GC TGG GAC GTG	GAG TGC GAT 144
Lys Lys Trp	Asn Ala Val	Ala Met Trp S	Ser Trp Asp Val	Glu Cys Asp
35		40	45	

- ACG AGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT

  Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

  60
- CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT
  Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
  65 70 75 80
- AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC
  Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

` C	90	0.0
35	90	9:

		s Gln Gln	GAC TGG GTG Asp Trp Val 105		g Ile Gly	336
AAA TGAGAG Lys	rggt tagaago	GCTT CTTAGC	GCAG TTGTTCA	AGAG CCCTGGT	FGGA	389
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG	449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT	509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC	569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT	629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT	689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT	749
TTAAA						754

### (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 105

Lys

#### (2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 754 base pairs

  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION:1..339
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide

### (B) LOCATION: 1...339

	(xi)	SE	QUENC	CE DI	ESCR	[PTIC	ON: S	SEQ I	D NO	): 27	7:						
														TCT Ser 15			48
														TCC Ser			96
														TGC Cys			144
														AGA Arg			192
														GAA Glu			240
														CAG Gln 95			288
														ATC Ile			336
AAA Lys	TGAC	GAGT	GGT 7	ΓAGA	AGGC'	rt C	rtag(	CGCA	TT(	GTTC <i>I</i>	AGAG	CCC	rggt	GGA			389
TCTT	rgta <i>i</i>	ATC (	CAGTO	GCCC.	га С	AAAG	GCTAC	AA(	CACTA	ACAG	GGG	ATGAZ	ATT (	CTTC	ATAAA	.G	449
GAGO	CCGAT	rgg Z	ATCTO	GTGG	rc T	rtgg/	ACTC	A TC	AAAGO	CCTT	GGT	ragc <i>i</i>	ATT '	rgrc <i>i</i>	AGTTT	т	509
ATCT	TCAC	GAA A	ATTC	rctg:	rg A	PAAT	GAAGA	A TAZ	ATTT	ATTA	AAG	GTGG:	rcc '	TTCC:	PACCT	C.	569
TGTO	GTGT	rgt (	GTCG	CGCA	CA C	AGCT	raga <i>i</i>	A GTO	GCTA:	ГААА	AAA	GGAA/	AGA (	GCTC	TAAAT	T	629
GAAT	CAC	CTT A	ATAAT	TTTA	CC CZ	ATTT(	CTATA	A CAZ	ACAGO	GCAG	TGG	AAGC	AGT '	TTCG	AGACT	Т	689
TTTC	CGATO	GCT 1	ratg(	GTTG2	AT C	AGTT	AAAA	A AG	AATG	TAC	AGT	AACA	TAA	AAAG	rgcag	T	749
TTAZ	A.A																754

# (2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15 . .

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp \$45\$

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys  $50 \\ \phantom{00}$  55

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 105 Lys (2) INFORMATION FOR SEQ ID NO: 29: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 754 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..339 (ix) FEATURE: (A) NAME/KEY: mat\_peptide (B) LOCATION: 1..339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29: ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 96 2.0 AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT 144 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA AGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser 240 AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 288 AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 336 100 105 389 AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449 GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509 ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569 TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629

689

749

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT

754 TTAAA

(2)	INFORMATION	FOR	SEQ	ID	NO:	30:
-----	-------------	-----	-----	----	-----	-----

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 105 100

Lys

### (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 754 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION:1..339
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 1..339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC	•	48
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His		
1				5					10					15			

- TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC 96 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30
- AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45144
- ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT 192 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
- CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT 240

G1n 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80	
														CAG Gln 95		288
														ATC Ile	GGC Gly	336
AAA Lys	TGAC	GAGT(	GGT 1	raga <i>i</i>	AGGC:	rt C	TAGO	CGCAC	3 TT(	GTTC#	AGAG	ccc	rggt(	GGA		389
TCTI	GTA	ATC (	CAGTO	GCCT	ra ca	AAAGO	CTAC	AAC	CACTA	ACAG	GGG	ATGAZ	ATT (	CTTC	AAATAG	449
GAGC	CGAT	rgg 2	ATCTO	GTGGT	rc T	rtgga	ACTC#	A TC	AAAGO	CCTT	GGT	ragc <i>i</i>	ATT '	TGTC	AGTTTT	509
ATCI	TCAC	GAA A	ATTC	rctg:	rg Ar	rtaa(	GAAGA	A TAZ	\TTT <i>I</i>	ATTA	AAG	GTGG	rcc '	TTCC:	PACCTO	569
TGTO	GTGT	rgt (	GTCG	CGCAC	CA CA	AGCT	ragaz	A GTO	GCTAT	AAA	AAA	GAA	AGA (	GCTC	CAAATT	629
GAAT	CAC	CTT A	ATAAT	PTTAC	CC CZ	ATTT(	TATA	A CA	ACAGO	GCAG	TGG	AAGC	AGT '	TTCG	AGACTT	689
тттс	GATO	GCT 1	ratg(	STTG!	AT C	AGTT	\AAA!	A AGA	AATGT	TAC	AGT	AACA	AAT .	AAAG'	rgcagt	749
TTA	λA															754

### (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80

Asn Lys Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

### (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 754 base pairs

  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1...339

# (ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION:1..339

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15	48
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	144
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60	192
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	240
AAT CAT TCC TTC AAG AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95	288
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110	336
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys	389
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

### (2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp \$45\$

Thr	Cys 50	Ala	Ile	Суѕ	Arg	Val 55	Gln	Val	Met	Asp	Ala 60	Cys	Leu	Arg	Cys	
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80	
Asn	His	Ser	Phe	Lys 85	Asn	Cys	Cys	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn	
Asn	Arg	Cys	Pro 100	Leu	Cys	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly	
Lys																
(2)	INF	ORMA	rion	FOR	SEQ	ID 1	10: 3	35:								
	(i)	(1 (1	A) L1 B) T1 C) S1	ENGTI YPE : FRANI	HARAC H: 75 nuc DEDNI DGY:	54 ba leic ESS:	ase p acio doul	pair:	5							
	(ii)	) MOI	LECUI	LE T	YPE:	CDN	A									
	(ix)		A) N	AME/I	KEY: ION: 1		39									
	(ix)		A) N	AME/	KEY:			tide								
	(xi	) SE	QUEN	CE D	ESCR:	IPTI	ON: :	SEQ :	ID NO	D: 3!	5:					
					GAC Asp											48
					TCC Ser											96
AAG Lys	AAG Lys	TGG Trp 35	AAC Asn	GCG Ala	GTG Val	GCC Ala	ATG Met 40	TGG Trp	AGC Ser	TGG Trp	GAC Asp	GTG Val 45	GAG Glu	TGC Cys	GAT Asp	144
					AGG Arg											192
CAA Gln 65	GCT Ala	GAA Glu	AAC Asn	AAA Lys	CAA Gln 70	GAG Glu	GAC Asp	TGT Cys	GTT Val	GTG Val 75	GTC Val	TGG Trp	GGA Gly	GAA Glu	TGT Cys 80	240
AAT Asn	CAT His	TCC Ser	TTC Phe	CAC His 85	AAC Asn	TGC Cys	AGC Ser	ATG Met	TCC Ser 90	CTG Leu	TGG Trp	GTG Val	AAA Lys	CAG Gln 95	AAC Asn	288
					TGC Cys											336
AAA Lys	TGA	GAGT	GGT '	TAGA	AGGC'	PT C	rtag(	CGCA	G TT	GTTC	AGAG	CCC'	rggt	GGA		389
TCT'	rgta.	ATC (	CAGT	GCCC'	TA C	AAAG(	GCTA	G AA	CACT	ACAG	GGG.	ATGA	ATT (	CTTC	AAATAG	449
GAG	CCGA'	TGG 2	ATCT	GTGG'	TC T	TTGG.	ACTC.	A TC	AAAG	CCTT	GGT	TAGC	ATT '	TGTC	AGTTTT	509
															TACCTO	

TTAAA	754
(2) INFORMATION FOR SEQ ID NO: 36:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 113 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	
<pre>(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:</pre>	
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	
Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn 85 90 95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105	
Lys	
(2) INFORMATION FOR SEQ ID NO: 37:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 754 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1339	
<pre>(ix) FEATURE:     (A) NAME/KEY: mat_peptide     (B) LOCATION:1339</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:	
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15	48
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	144

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT

TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT

689

749

ACG TGC ( Thr Cys 1 50													192
CAA GCT ( Gln Ala ( 65			n Glu										240
AAT CAT Asn His S													288
AAT CGC A Asn Arg S													336
AAA TGAGA Lys	AGTGGT 1	ragaagg	CTT C	ГТАGC	CGCAC	TTC	STTC <i>I</i>	AGAG	CCCI	GGT(	GGA		389
TCTTGTAA	TC CAGTO	GCCCTA	CAAAG	GCTAC	AAC	CACTA	ACAG	GGG	TGA	ATT (	CTTC	\AATAG	449
GAGCCGAT	GG ATCT	GTGGTC	TTTGG	ACTC	A TC	AAAGO	ССТТ	GGTT	AGC	TT.	rgtca	AGTTTT	509
ATCTTCAG	AA ATTC	TCTGTG	ATTAA	GAAGA	A TAA	ATTTA	ATTA	AAGO	TGG7	rcc :	rtcci	TACCTC	569
TGTGGTGT	GT GTCG	CGCACA	CAGCT	raga <i>i</i>	A GTO	CTAT	AAA	AAAC	GAA	AGA (	GCTCC	CAAATT	629
GAATCACC'	TT ATAA	TTTACC	CATTT	CTATA	A CAA	ACAGO	GCAG	TGG	AAGC	AGT :	rtcg/	AGACTT	689
TTTCGATG	CT TATG	GTTGAT	CAGTT	AAAA	A AGA	AATGT	TAC	AGT	AACAZ	AT A	AAAG:	rgcagt	749
TTAAA													754

### (2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

# (2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 754 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double (D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: cDNA

ı	/ i	v١	1	PE.	Δ	וח	īR	E	

(A) NAME/KEY: CDS

(B) LOCATION:1..339

# (ix) FEATURE:

(A) NAME/KEY: mat\_peptide
(B) LOCATION:1..339

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15	48
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35	144
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60	192
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	240
AAT AAA TCC TTC AAG AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85	288
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105	336
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys	389
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATA	AG 449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT	T 509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCT	C 569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAAT	T 629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACT	TT 689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAG	FT 749
TTAAA	754

# (2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

20 25

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 45Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys 65 70 75 80 Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

### (2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 754 base pairs
    (B) TYPE: nucleic acid

  - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION:1..339
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide (B) LOCATION:1..339

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

								GAA Glu							48.
								GGA Gly 25							96
								TGG Trp							144
								GTG Val							192
								TGT Cys							240
								ATG Met							288
								GAC Asp 105							336
AAA Lys	TGA	GAGT(	GGT 5	raga <i>i</i>	AGGC	rt C	rtag(	CGCA	G TT(	GTTC	AGAG	CCC	rggt(	GGA	389

TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG

449

GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT	509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC	569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT	629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT	689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT	749
TTAAA						754

# (2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 105

Lys

# (2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 754 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1...339
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 1...339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 48

TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu

96

AAG A Lys I																144
ACG T	_															192
CAA ( Gln 2 65																240
AAT ( Asn I			_		_											288
AAT ( Asn <i>l</i>																336
AAA T	TGAG	SAGT	GGT 1	raga <i>i</i>	AGGCT	rr Ci	TTAG(	CGCAC	TTC	TTC?	AGAG	CCCI	GGT	GGA		389
TCTT	GTAA	TC (	CAGTO	GCCCI	ra ca	AAAGO	GCTAC	AAC	CACTA	ACAG	GGG	TGAZ	ATT (	CTTCA	AATAG	449
GAGC	CGAT	rgg i	ATCT	GTGG7	rc T	rtgg <i>i</i>	ACTC	A TC	AAAG	ССТТ	GGTT	ragc <i>i</i>	ATT I	rgtc <i>i</i>	AGTTTT	509
ATCT'	TCAC	SAA A	ATTC	rctgi	rg An	)AATI	GAAGA	A TAZ	ATTT?	ATTA	AAGO	GTGGT	rcc r	rtcci	PACCTC	569
TGTG	GTGI	GT (	GTCG	CGCAC	CA CA	AGCTT	ragàa	A GTO	CTAT	гааа	AAAC	GAAA	AGA (	GCTCC	CAAATT	629
GAAT	CACC	CTT Z	ATAAT	PTTA(	CC CZ	ATTTO	TATA	A CA	ACAGO	GCAG	TGG	AAGC	AGT :	rTCG <i>I</i>	GACTT	689
TTTC	GATO	CT '	ratgo	GTTG <i>I</i>	AT C	AGTT?	AAAA	A AGA	ATG?	TAC	AGT	AACA	AAT A	AAAGT	TGCAGT	749
TTAA	A															754

#### (2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids (B) TYPE: amino acid

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp \$35\$

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50

Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn  $85 \hspace{1cm} 90 \hspace{1cm} 95$ 

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

### (2) INFORMATION FOR SEQ ID NO: 45:

(i)	SEOUENCE	CHARACTERISTICS:

- EQUENCE CHARACTERISTICS:

  (A) LENGTH: 754 base pairs

  (B) TYPE: nucleic acid

  (C) STRANDEDNESS: double

  (D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: cDNA

# (ix) FEATURE:

- (A) NAME/KEY: CDS
  (B) LOCATION:1..339

# (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
  (B) LOCATION:1..339

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 5 10 15	48							
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30	96							
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp 35 40 45	144							
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA AGT Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser 50 55 60	192							
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80	240							
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95	288							
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110	336							
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA Lys								
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449							
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509							
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569							
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629							
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689							
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749							
TTAAA	754							

# (2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 113 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met 1	Ala	Asp	Val	Glu 5	Asp	Gly	Glu	Glu	Thr 10	Cys	Ala	Leu	Ala	Ser 15	His	
Ser	Gly	Ser	Ser 20	Gly	Ser	Lys	Ser	Gly 25	Gly	Asp	Lys	Met	Phe 30	Ser	Leu	
Lys	Lys	Trp 35	Asn	Ala	Val	Ala	Met 40	Trp	Ser	Trp	qaA	Val 45	Glu	Cys	Asp	
Thr	Cys 50	Ala	Ile	Cys	Arg	Val 55	Gln	Val	Met	Asp	Ala 60	Ser	Leu	Arg	Ser	
Gln 65	Ala	Glu	Asn	Lys	Gln 70	Glu	Asp	Cys	Val	Val 75	Val	Trp	Gly	Glu	Cys 80	
Asn	His	Ser	Phe	His 85	Asn	Cys	Cys	Met	Ser 90	Leu	Trp	Val	Lys	Gln 95	Asn	
Asn	Arg	Cys	Pro 100	Leu	Cys	Gln	Gln	Asp 105	Trp	Val	Val	Gln	Arg 110	Ile	Gly	
Lys																
(2)	INFO	ORMAT	NOI	FOR	SEQ	ID 1	10: 4	17:								
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 754 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear																
	(ii) MOLECULE TYPE: cDNA															
	(ix)		A) NA	AME/I			39									
(B) LOCATION:1339  (ix) FEATURE:  (A) NAME/KEY: mat_peptide  (B) LOCATION:1339																
	(xi)	) SE	QUEN	CE DI	ESCR:	[PTI	ON:	SEQ :	ID NO	O: 4'	7:					
ATG Met 1	GCC Ala	GAC Asp	GTG Val	GAA Glu 5	GAC Asp	GGA Gly	GAG Glu	GAA Glu	ACC Thr 10	TGC Cys	GCC Ala	CTG Leu	GCC Ala	TCT Ser 15	CAC His	48
TCC Ser	GGG Gly	AGC Ser	TCA Ser 20	Gly	Ser	Lys	Ser	Gly	Gly	GAC Asp	Lys	Met	TTC Phe 30	TCC Ser	CTC Leu	96
AAG Lys	AAG Lys	TGG Trp 35	Asn	GCG Ala	GTG Val	GCC Ala	ATG Met 40	TGG Trp	AGC Ser	TGG Trp	GAC Asp	GTG Val 45	GAG Glu	TGC Cys	GAT Asp	144
	TGC Cys 50															192
	GCT Ala															240
AAT Asn	CAT His	TCC Ser	TTC Phe	CAC His 85	AAC Asn	TGC Cys	TGC Cys	ATG Met	TCC Ser 90	CTG Leu	TGG Trp	GTG Val	AAA Lys	CAG Gln 95	AAC Asn	288
	CGC Arg															336

AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA

TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG	449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT	509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC	569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT	629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TTCGAGACTT	689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT	749
TTAAA						754

### (2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn

Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100

Lys

# (2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 754 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..339
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 1...339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1				5					10					15			
TCC Ser	GGG Gly	AGC Ser	TCA Ser 20	GGC Gly	TCC Ser	AAG Lys	TCG Ser	GGA Gly 25	GGC Gly	GAC Asp	AAG Lys	ATG Met	TTC Phe 30	TCC Ser	CTC Leu		96
AAG Lys	AAG Lys	TGG Trp 35	AAC Asn	GCG Ala	GTG Val	GCC Ala	ATG Met 40	TGG Trp	AGC Ser	TGG Trp	GAC Asp	GTG Val 45	GAG Glu	AGC Ser	GAT Asp		144
ACG Thr	TGC Cys 50	GCC Ala	ATC Ile	TGC Cys	AGG Arg	GTC Val 55	CAG Gln	GTG Val	ATG Met	GAT Asp	GCC Ala 60	TGT Cys	CTT Leu	AGA Arg	TGT Cys		192
CAA Gln 65	GCT Ala	GAA Glu	AAC Asn	AAA Lys	CAA Gln 70	GAG Glu	GAC Asp	TGT Cys	GTT Val	GTG Val 75	GTC Val	TGG Trp	GGA Gly	GAA Glu	TGT Cys 80		240
AAT Asn	CAT His	TCC Ser	TTC Phe	CAC His 85	AAC Asn	TGC Cys	TGC Cys	ATG Met	TCC Ser 90	CTG Leu	TGG Trp	GTG Val	AAA Lys	CAG Gln 95	AAC Asn		288
AAT Asn	CGC Arg	TGC Cys	CCT Pro 100	CTC Leu	TGC Cys	CAG Gln	CAG Gln	GAC Asp 105	TGG Trp	GTG Val	GTC Val	CAA Gln	AGA Arg 110	ATC Ile	GGC Gly		336
AAA Lys	TGA	GAGT	GGT 1	raga <i>i</i>	AGGC	rt C	rtag(	CGCA	G TTC	GTTC1	AGAG	CCC	rggt(	GGA			389
TCT	rgta <i>i</i>	ATC (	CAGT	GCCC'	ra c	AAAG	GCTA(	G AAG	CACT	ACAG	GGG	ATGAZ	ATT (	CTTC	AAATAG	;	449
GAG	CCGA	rgg 2	ATCT	GTGG'	rc T	rtgg:	ACTC	A TC	AAAG	CCTT	GGT'	ragc:	TTA	TGTC	AGTTTI	,	509
ATC	TTCA	GAA A	ATTC'	TCTG	rg a	rtaa(	GAAG	A TA	ATTTA	ATTA	AAG	GTGG'	rcc '	TTCC'	PACCTO	:	569
TGT	GGTG'	rgt (	GTCG	CGCA	CA C	AGCT'	raga <i>i</i>	A GT	GCTA:	raaa	AAA	GGAA	AGA (	GCTC	CAAATI		629
GAA'	rcac(	CTT A	ATAA'	TTTA	cc c	ATTT	CTATA	A CA	ACAG	GCAG	TGG.	AAGC	AGT '	TTCG	AGACTT		689
TTTC	CGAT	GCT '	TATG	GTTG	AT C	AGTT	AAAA	A AG	AATG'	TTAC	AGT	AACA	AAT A	AAAG'	rgcagī		749
TTA	AA																754

# (2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His 1 10 15

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu 20 25 30

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp 35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys 50 55 60

Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys 65 70 75 80

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn 85 90 95 .

Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly 100 105 110

Cont Lys

30